

1 ATGCTGTTCCGCGCCCGGGGCGGTACGGGGCAGGGGCTGGGGCGGCCCGCGGAGGCT 60
1 M L F R A R G P V R G R G W G R P A E A 20
61 CCCCCGCGCGGGCGCTCGCCGCCCTGGAGCCCCGCTGGATTGCTGCTGGGCGCTCGGC 120
21 P R R G R S P P W S P A W I C C W A L A 40
121 GGCTGCCAGGCGGCCTGGGCTGGGGACCTGCCCTCCTCCTCCAGCCGCCCGCTTCCTCCT 180
41 G C Q A A W A G D L P S S S S R P L P P 60
181 TGCCAGGAGAAAGATTATCACTTTGAATATACGGAATGTGATAGCACTGGCTCCAGGTGG 240
61 C Q E K D Y H F E Y T E C D S S G S R W 80
241 AGAGTTGCCATTCCAAATTCTGCAGTGGACTGCTCTGGCCTGCCTGACCCAGTGAGAGGC 300
81 R V A I P N S A V D C S G L P D P V R G 100
301 AAAGAATGCACTTTCTCCTGTGCTTCTGGAGAGTATCTAGAAATGAAGAACCAGGTATGC 360
101 K E C T F S C A S G E Y L E M K N Q V C 120
361 AGTAAGTGTGGTGAAGGCACCTATTCCTTGGGCAGTGGCATCAAATTTGATGAATGGGAT 420
121 S K C G E G T Y S L G S G I K F D E W D 140
421 GAATTGCCGGCAGGATTTTCTAACATCGCAACATTCATGGACACTGTGCTGGGCCCTTCT 480
141 E L P A G F S N I A T F M D T V V G P S 160
481 GACAGCAGGCCAGACGGCTGTAACAACTCTTCTTGGATCCCTCGTGGAACACTACATAGAA 540
161 D S R P D G C N N S S W I P R G N Y I E 180
541 TCTAATCGTGATGACTGCACGGTGTCTTTGATCTATGCTGTGCACCTTAAGAAGTCAGGC 600
181 S N R D D C T V S L I Y A V H L K K S G 200
601 TATGTCTTCTTTGAGTACCAGTATGTCGACAACAACATCTTCTTTGAGTTCTTTATTCAA 660
201 Y V F F E Y Q Y V D N N I F F E F F I Q 220

FIG. 1A



661 AATGATCAGTCCCAGGAGATGGACACCACCACTGACAAGTGGGTAAACTTACAGACAAT 720
 221 N D Q C Q E M D T T T D K W V K L T D N 240

 721 GGAGAATCGGGCTCTCATTCTGTAATGCTGAAATCAGGCACAAACATACTCTACTGGAGA 780
 241 G E W G S H S V M L K S G T N I L Y W R 260

 781 ACTACAGGCATCCTTATGGGTTCTAAGGCGGTCAAGCCTGTGCTGGTAAAAAATATCACA 840
 261 T T G I L M G S K A V K P V L V K N I T 280

 841 ATTGAAGGGGTGGCGTACACATCAGAATGTTTTCTTGCAAGCCAGGCACATTCAGCAAC 900
 281 I E G V A Y T S E C F P C K P G T F S N 300

 901 AAACCAGGTTCAATCAACTGCCAGGTGTGTCCCAGAAACACCTATTCTGAGAAAGGAGCC 960
 301 K P G S F N C Q V C P R N T Y S E K G A 320

 961 AAAGAATGTATAAGGTGTAAAGACGACTCTCAATTTTCAGGATCCAGTGAGTGACAGAG 1020
 321 K E C I R C K D D S Q F S G S S E C T E 340

 1021 CGCCCTCCCTGTACCACAAAAGACTATTTCCAGATCCATACTCCATGTGATGAAGAAGGA 1080
 341 R P P C T T K D Y F Q I H T P C D E E G 360

 1081 AAGACACAGATAATGTACAAGTGGATAGAGCCCAAATCTGCCGGGAGGATCTCACAGAT 1140
 361 K T Q I M Y K W I E P K I C R E D L T D 380

 1141 GCTATTAGATTGCCCCCTTCTGGAGAGAAGAAGGATTGTCCGCCTTGCAACCCTGGATTT 1200
 381 A I R L P P S G E K K D C P P C N P G F 400

 1201 TATAACAATGGATCATCTTCTTGCCATCCCTGTCTCCTGGAACATTTTCAGATGGAACC 1260
 401 Y N N G S S S C H P C P P G T F S D G T 420

 1261 AAAGAATGTAGACCATGTCCAGCAGGAACGGAGCCTGCACTTGGCTTTGAATATAAATGG 1320
 421 K E C R P C P A G T E P A L G F E Y K W 440

FIG. 1B



1321 TGAATGTCCTTCCTGGCAACATGAAAACCTCCTGCTTCAATGTTGGGAATTCAAAGTGC 1380
 441 W N V L P G N M K T S C F N V G N S K C 460

1381 GATGGAATGAATGGTTGGGAGGTGGCTGCAGATCATATCCAGAGTGGGGCTGGAGGTTCT 1440
 461 D G M N G W E V A G D H I Q S G A G G S 480

1441 GACAATGATTACCTGATCTTAAACTTGCATATCCCAGGATTTAAACCACCAACATCTATG 1500
 481 D N D Y L I L N L H I P G F K P P T S M 500

1501 ACTGCAGCCACGGGTTCTGAACTAGGAAGAATAACATTTGTCTTTGAGACCCTCTGTTCA 1560
 501 T G A T G S E L G R I T F V F E T L C S 520

1561 GCTGACTGTGTTTTGTACTTCATGGTGCATATTAATAGAAAAAGTACAAATGTGGTAGAA 1620
 521 A D C V L Y F M V D I N R K S T N V V E 540

1621 TCGTGGGGTGAACCAAAGAAAAACAAGCTTACACCCATATCATCTTCAAGAATGCAACT 1680
 541 S W G G T K E K Q A Y T H I I F K N A T 560

1681 TTTACATTTACATGGGCATTCCAGAGAACTAATCAGGGTCAAGATAATAGACGGTTCATC 1740
 561 F T F T W A F Q R T N Q G Q D N R R F I 580

1741 AATGACATGGTGAAGATTTATTCTATCACAGCCACTAATGCAGTTGATGGGGTGGCGTCC 1800
 581 N D M V K I Y S I T A T N A V D G V A S 600

1801 TCATGCCGTGCCTGTGCCCTCGGTTCTGAACAGTGGGTTTCATCGTGTGTCCCCTGCCCT 1860
 601 S C R A C A L G S E Q S G S S C V P C P 620

1861 CCAGGCCACTACATTGAGAAAGAAACCAACCAGTGCAAGGAATGTCCACCTGACACCTAC 1920
 621 P G H Y I E K E T N Q C K E C P P D T Y 640

1921 CTGTCCATACATCAGGTCTATGGCAAAGAGGCTTGTATTCCATGCGGGCCTGGCAGTAAA 1980
 641 L S I H Q V Y G K E A C I P C G P G S K 660

FIG. 1C



1981 AACAAATCAGGACCATTTCGGTTTGCTATAGTGACTGCTTTTTCTACCATGAAAAAGAAAAT 2040
 661 N N Q D H S V C Y S D C F F Y H E K E N 680
 2041 CAGATTTTGCACCTATGACTTTAGCAACCTCAGCAGTGTGGGCTCATTAAATGAATGGCCCC 2100
 681 Q I L H Y D F S N L S S V G S L M N G P 700
 2101 AGCTTCACCTCCAAAGGAACAAAATACTTCCATTTCTTCAATATCAGTTTATGTGGGCAT 2160
 701 S F T S K G T K Y F H F F N I S L C G H 720
 2161 GAGGGAAGAAGATGGCTCTCTGTACCAACAATATAACAGACTTTACAGTAAAAGAAATA 2220
 721 E G K K M A L C T N N I T D F T V K E I 740
 2221 GTGGCAGGGTCAGATGATTACACAAATTTGGTAGGGGCATTTGTATGCCAGTCAACAATT 2280
 741 V A G S D D Y T N L V G A F V C Q S T I 760
 2281 ATTCCTTCTGAAAGTAAGGGTTTCCGAGCAGCCTTATCATCACAATCCATCATTCTGGCA 2340
 761 I P S E S K G F R A A L S S Q S I I L A 780
 2341 GATACATTCATAGGAGTCACAGTTGAAACCACATTGAAAAATATTAATATAAAAGAAGAT 2400
 781 D T F I G V T V E T T L K N I N I K E D 800
 2401 ATGTTCCCAGTTCCAACAAGCCAAATACCAGATGTGCATTTCTTTTATAAGTCTTCTACA 2460
 801 M F P V P T S Q I P D V H F F Y K S S T 820
 2461 GCAACAACATCTTGTATTAATGGCCGATCAACTGCTGTGAAAATGAGGTGTAATCCTACT 2520
 821 A T T S C I N G R S T A V K M R C N P T 840
 2521 AAATCTGGAGCAGGAGTGATTTTCAGTCCCCAGCAAGTGGCCAGCAGGTACCTGTGATGGG 2580
 841 K S G A G V I S V P S K C P A G T C D G 860
 2581 TGTACGTTCTATTTCTGTGGGAGAGTGCTGAAGCTTGCCCTCTGTGTACGGAGCATGAC 2640
 861 C T F Y F L W E S A E A C P L C T E H D 880

FIG. 1D



2641 TTCCATGAGATTGAGGGAGCCTGCAAGAGAGGATTCAGGAAACCTTGTATGTGTGGAAT 2700
 881 F H E I E G A C K R G F Q E T L Y V W N 900
 2701 GAACCTAAATGGTGCATTAAACGAATTTCTTTGCCTGAGAAAAAGTTGGCAACCTGTGAA 2760
 901 E P K W C I K G I S L P E K K L A T C E 920
 2761 ACGGTTGACTTTTGGCTGAAGGTGGGAGCCGGTGTGGGAGCTTTTACTGCCGTTTTCCTG 2820
 921 T V D F W L K V G A G V G A F T A V L L 940
 2821 GTGGCTCTGACCTGCTACTTCTGAAAAAGAATCAAAGAAAAAGAAGACCATTTTGAAT 2880
 941 V A L T C Y F W K K N Q K K K K T I L N 960
 2881 CTGTTCAACTGAAAACCTCAAGATCCCCAAATATATGAAGAGACAGTGCTGTAGCCTTCA 2940
 961 L F N * 964
 2941 GACTAATGAACAAAGAAACCTGCTCTAGTTTTACAGGACCATATTTTAGGGTCTGTCCTC 3000
 3001 ATACCTGTCACATTGGTGATCTCACAGAGGAGGGCCATGCCGCTGAAAAGGGAAGGAGAT 3060
 3061 TGAAACATTTGATTGCCTTATCACATGGTCAAGTACCTTGCCAAATAAAGCAAAGCAAAT 3120
 3121 GATTTGGGTCTCAACTGAAGATGAAGCTCAACTCAGGAAGAGATTTATCTGTATATACAC 3180
 3181 ATAAGTGAACCAAGTTTAAAGCCACCAATGCACTGCTGATGCATGCCATATAATTAAT 3240
 3241 GGGTAACTTTTATTCTTTATGATGTCTACATAACAAGTGTGATTTGGAAGGCACATGTGA 3300
 3301 GCATATGCATTATGATCCAATTTATGTTTTTCTTTGTTTATATTTTGGGGAAAATTAAA 3360
 3361 ATTTTTTTAAGGTAAAAAAAAAAAAAAAAAAAA 3390

FIG. 1E



FIG. 2A

		10	20	30																												
1	M	L	F	R	A	G	P	V	R	G	R	G	W	G	R	P	A	E	A	P	R	R	G	R	S	P	F	W	S	TR16.aa		
1	M	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	EMB	CAB41042.1 TNFR
1	M	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	emb	CAA53576.1 OX40
		40	50	60																												
31	P	A	W	I	C	C	W	A	L	A	G	C	Q	A	A	W	A	G	D	L	P	S	S	S	S	R	B	L	P	TR16.aa		
10	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	EMB	CAB41042.1 TNFR
13	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	emb	CAA53576.1 OX40
		70	80	90																												
61	C	Q	E	K	D	Y	H	F	E	Y	T	E	C	D	S	S	G	S	R	W	R	V	A	I	P	N	S	A	V	D	TR16.aa	
23	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	EMB	CAB41042.1 TNFR
26	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	emb	CAA53576.1 OX40
		100	110	120																												
91	C	S	G	L	P	D	E	V	R	G	K	E	C	T	F	S	C	A	S	G	E	Y	L	E	M	K	N	O	V	C	TR16.aa	
30	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	EMB	CAB41042.1 TNFR
31	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	emb	CAA53576.1 OX40
		130	140	150																												
121	S	K	C	G	E	G	T	Y	S	L	G	S	G	I	K	F	D	E	W	D	E	L	P	A	G	F	S	N	I	A	TR16.aa	
51	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	EMB	CAB41042.1 TNFR
43	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	emb	CAA53576.1 OX40
		160	170	180																												
151	T	F	M	D	T	V	G	P	S	D	S	R	P	D	G	C	N	N	S	S	W	I	P	R	G	N	Y	I	E	TR16.aa		
51	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	EMB	CAB41042.1 TNFR
43	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	emb	CAA53576.1 OX40
		190	200	210																												
181	S	N	R	D	D	C	T	V	S	L	I	Y	A	V	H	L	K	K	S	G	V	F	F	E	Y	O	Y	V	D	TR16.aa		
51	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	EMB	CAB41042.1 TNFR
43	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	emb	CAA53576.1 OX40
		220	230	240																												
211	N	N	I	F	F	E	F	F	I	O	N	D	Q	C	Q	E	M	D	T	T	T	D	K	W	V	K	L	T	D	N	TR16.aa	
51	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	EMB	CAB41042.1 TNFR
43	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	emb	CAA53576.1 OX40
		250	260	270																												
241	G	E	W	G	S	H	S	V	M	L	K	S	G	T	N	I	L	Y	W	R	T	T	G	I	L	M	G	S	K	A	TR16.aa	
51	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	EMB	CAB41042.1 TNFR
43	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	emb	CAA53576.1 OX40
		280	290	300																												
271	V	K	P	V	L	V	K	N	I	T	E	G	V	A	Y	T	S	E	C	F	P	C	K	P	G	T	F	S	N	TR16.aa		
51	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	EMB	CAB41042.1 TNFR
43	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	emb	CAA53576.1 OX40
		310	320	330																												
301	K	P	G	S	F	N	C	O	V	C	P	R	N	T	Y	S	E	K	G	A	K	E	C	I	R	C	K	D	D	S	TR16.aa	
62	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	EMB	CAB41042.1 TNFR
54	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	emb	CAA53576.1 OX40

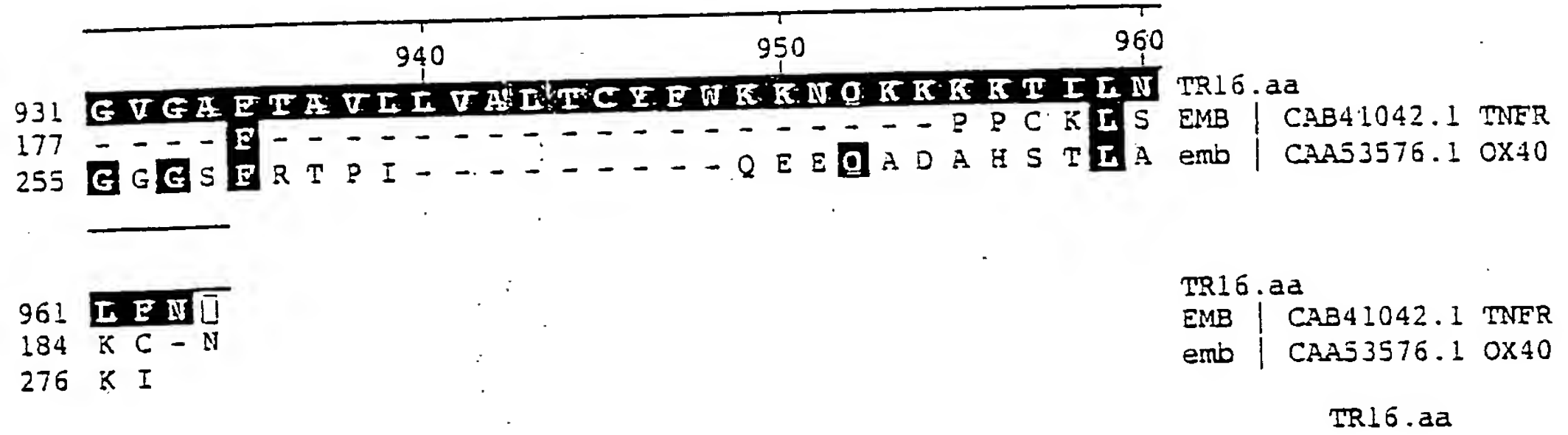
FIG. 2B

		340		350		360																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																													
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70	T	K	C	E	R	C	P	P	H	T	Y	T	A	I	P	N	Y	S	N	G	C	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-

FIG. 2C

		640	650	660		
631	O C K E C P P D T Y L S P H O V Y G K E A C I F C G P G S K				TR16.aa	
147	- - - - -			G G I	EMB	CAB41042.1 TNFR
134	- - - - -			S P G	emb	CAA53576.1 OX40
		670	680	690		
661	N N Q D H S V C Y S D C F F Y H E K E N Q I L H Y D F S N L				TR16.aa	
150	D E Q G N P I C				EMB	CAB41042.1 TNFR
137	D N Q A - - - C				emb	CAA53576.1 OX40
		700	710	720		
691	S S V G S I M N G P S F T S K G T K Y F F E F N I S L C G H				TR16.aa	
158	- - - - - K S			C C V	EMB	CAB41042.1 TNFR
142	- - - - - K P W T N			C T L	emb	CAA53576.1 OX40
		730	740	750		
721	E G K R M A L C T N N I T D F T V K E I V A G S D D Y T N L				TR16.aa	
163	G E - - - - - Y				EMB	CAB41042.1 TNFR
150	A G K H - - - - - T L Q P A S N S S D A I				emb	CAA53576.1 OX40
		760	770	780		
751	V G A F V C O S T I I P S E S K G F R A A L S S O S I I L A				TR16.aa	
166	- - - - - C D				EMB	CAB41042.1 TNFR
166	- - - - - C E D R D P E A T Q P Q E T Q G P P A R P I T V Q				emb	CAA53576.1 OX40
		790	800	810		
781	D T F I G V T V E T T L K N I N I K E D M F P V P T S O I P				TR16.aa	
168	- - - - -				EMB	CAB41042.1 TNFR
191	P T - - - - - E A W P - R T S Q G P				emb	CAA53576.1 OX40
		820	830	840		
811	D V H F F Y K S S T A T E S C I N G R S T A V K M R C N P T				TR16.aa	
168	- - - - -				EMB	CAB41042.1 TNFR
203	- - - - - S T R P V E V P G G R A V A A I L				emb	CAA53576.1 OX40
		850	860	870		
841	K S G A G V I S V P S K C P A G T C D G C T F Y F L W E S A				TR16.aa	
168	- - - - -				EMB	CAB41042.1 TNFR
220	- - - - - G L G L V - - - - - L G L L				emb	CAA53576.1 OX40
		880	890	900		
871	E A C P L C T E H D F H E I E G A C K T G F O E T L Y V W N				TR16.aa	
168	- - - - -				EMB	CAB41042.1 TNFR
229	- - - - - G P L - - - - - A I L L A L Y L L R				emb	CAA53576.1 OX40
		910	920	930		
901	E P K W C I K G I S L H E K K L A T C E T V D F W L K V G A				TR16.aa	
170	- - - - - R N Y R L D P				EMB	CAB41042.1 TNFR
242	- - - - - R D Q R L E P D A H K P				emb	CAA53576.1 OX40

FIG. 2D



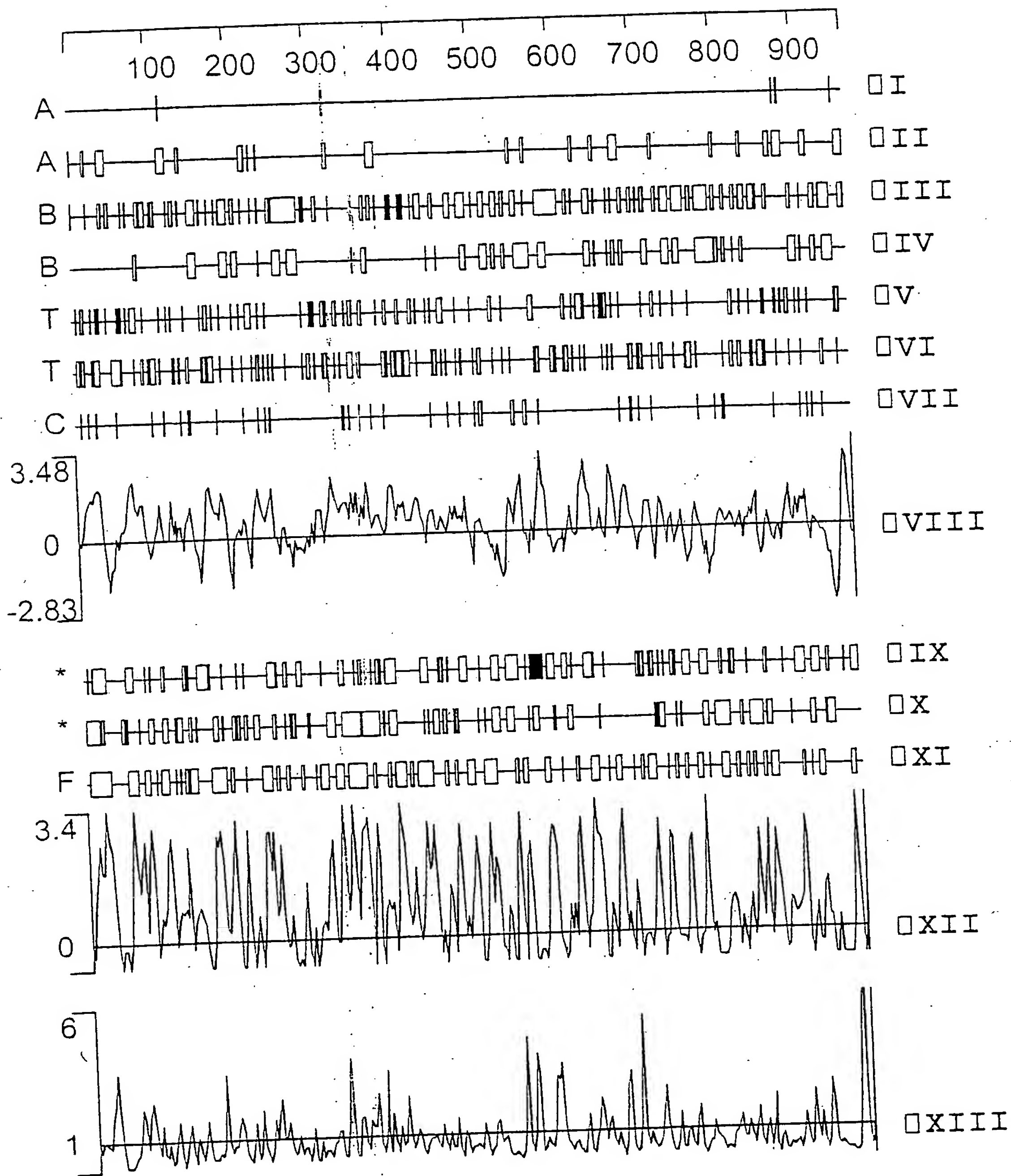


FIG. 3

1 ATGCTGTTCCGCGCCCGGGGGCCGTACGGGGCAGGGCTGGGGGCGCCGCGGAGGCT 60
 1 M L F R A R G P V R G R G W G R P A E A 20

 61 CCCC GCCGCGGGCGCTCGCCGUCCTGGAGCCCCGCCTGGATTGCTGCTGGGCGCTCGCC 120
 21 P R R G R S P P W S P A W I C C W A L A 40

 121 GGCTGCCAGGCGGCCTGGGCTGGGACCTGCCCTCCTCCTCCAGCCGCCGCTTCCTCCT 180
 41 G C Q A A W A G D L P S S S S R P L P P 60

 181 TGCCAGGAGAAAGATTATCACTTTGAATATACGGAATGTGATAGCAGTGGCTCCAGGTGG 240
 61 C Q E K D Y H F E Y T E C D S S G S R W 80

 241 AGAGTTGCCATTCCAAATTCTGCAGTGGACTGCTCTGGCCTGCCTGACCCAGTGAGAGGC 300
 81 R V A I P N S A V D C S G L P D P V R G 100

 301 AAAGAATGCACTTTCTCCTGTGCTTCTGGAGAGTATCTAGAAATGAAGAACCAGGTATGC 360
 101 K E C T F S C A S G E Y L E M K N Q V C 120

 361 AGTAAGTGTGGTGAAGGCACCTATTCCTTGGGCAGTGGCATCAAATTTGATGAATGGGAT 420
 121 S K C G E G T Y S L G S G I K F D E W D 140

 421 GAATTGCCCGCAGGATTTTCTAACATCGCAACATTCATCGACACTGTGGTGGGCCCTTCT 480
 141 E L P A G F S N I A T F M D T V V G P S 160

 481 GACAGCAGGCCAGACGGCTGTAACAACTCTTCTGGATCCCTCGTGAAACTACATAGAA 540
 161 D S R P D G C N N S S W I P R G N Y I E 180

 541 TCTAATCGTGATGACTGCACGGTGTCTTTGATCTATGCTGTGCACCTTAAGAAGTCAGGC 600
 181 S N R D D C T V S L I Y A V H L K K S G 200

 601 TATGTCTTCTTTGAGTACCAGTATGTCGACAACAACATCTTCTTTGAGTTCTTTATTCAA 660
 201 Y V F F E Y Q Y V D N N I F F E F F I Q 220

 661 AATGATCAGTGCCAGGAGATGGACACCACCACTGACAAGTGGGTAAAACTTACAGACAAT 720
 221 N D Q C Q E M D T T T D K W V K L T D N 240

FIG. 4A



721 GGAGAATGGGGCTCTCATTCTGTAATGCTGAAATCAGGCACAAACATACTCTACTGGAGA 780
 241 G E W G S H S V M L K S G T N I L Y W R 260
 781 ACTACAGGCATCCTTATGGGTTCTAAGGCGGTCAAGCCTGTGCTGGTAAAAATATCACA 840
 261 T T G I L M G S K A V K P V L V K N I T 280
 841 ATTGAAGGGGTGGCGTACACATCAGAATGTTTTCCTTGCAAGCCAGGCACATTCAGCAAC 900
 281 I E G V A Y T S E C F P C K P G T F S N 300
 901 AAACCAGGTTTCACTCACTGCCAGGTGTGTCCCAGAAACACCTATTCTGAGAAAGGAGCC 960
 301 K P G S F N C Q V C P R N T Y S E K G A 320
 961 AAAGAATGTATAAGGTGTAAAGACGACTCTCAATTTTCAGGATCCAGTGAGTGACAGAG 1020
 321 K E C I R C K D D S Q F S G S S E C T E 340
 1021 CGCCCTCCCTGTACCACAAAAGACTATTTCCAGATCCATACTCCATGTGATGAAGAAGGA 1080
 341 R P P C T T K D Y F Q I H T P C D E E G 360
 1081 AAGACACAGATAATGTACAAGTGGATAGAGCCCAAATCTGCCGGGAGGATCTCACAGAT 1140
 361 K T Q I M Y K W I E P K I C R E D L T D 380
 1141 GCTATTAGATTGCCCCCTTCTGGAGAGAAGAAGATTGTCCGCCTTGCAACCCTGGATTT 1200
 381 A I R L P P S G E K K D C P P C N P G F 400
 1201 TATAACAATGGATCATCTTCTTGCCATCCCTGTCTCCTGGAACATTTTCAGATGGAACC 1260
 401 Y N N G S S S C H P C P P G T F S D G T 420
 1261 AAAGAATGTAGACCATGTCCAGCAGGAACGGAGCCTGCACTTGGCTTTGAATATAAATGG 1320
 421 K E C R P C P A G T E P A L G F E Y K W 440
 1321 TGAATGTCCTTCTGGAACATGAAAACCTTCTGCTTCAATGTTGGAATTCAAAGTGC 1380
 441 W N V L P G N M K T S C F N V G N S K C 460
 1381 GATGGAATGAATGGTTGGGAGGTGGCTGCAGATCATATCCAGAGTGGGGCTGGAGGTTCT 1440
 461 D G M N G W E V A G D H I Q S G A G G S 480

FIG. 4B



1441 GACAATCATTACCTGATCTTAAACTTGCATATCCCAGGATTTAAACCACCAACATCTATG 1500
 481 D N D Y L I L N L H I P G F K P P T S M 500

1501 ACTGGAGCCACGGTTCTGAACTAGGAAGAATAACATTTGTCTTTGAGACCCTCTGTTCA 1560
 501 T G A T G S E L G R I T F V F E T L C S 520

1561 GCTGACTGTGTTTTGTACTTCATCGTGGATATTAATAGAAAAAGTACAAATGTGGTAGAA 1620
 521 A D C V L Y F M V D I N R K S T N V V E 540

1621 TCGTGGGGTGAACCAAAGAAAAACAAGCTTACACCCATATCATCTTCAAGAATGCAACT 1680
 541 S W G G T K E K Q A Y T H I I F K N A T 560

1681 TTTACATTTACATGGGCATTCCAGAGAACTAATCAGGGTCAAGATAATAGACGGTTCATC 1740
 561 F T F T W A F Q R T N Q G Q D N R R F I 580

1741 AATGACATGCTGAAGATTTATTCTATCACAGCCACTAATGCAGTTGATGGGGTGGCGTCC 1800
 581 N D M V K I Y S I T A T N A V D G V A S 600

1801 TCATGCCGTGCCTGTGCCCTCGGTTCTGAACAGTCGGGTTTCATCGTGTGTCCCCTGCCCT 1860
 601 S C R A C A L G S E Q S G S S C V P C P 620

1861 CCAGGCCACTACATTGAGAAAGAAACCAACCAGTGAAGGAATGTCCACCTGACACCTAC 1920
 621 P G H Y I E K E T N Q C K E C P P D T Y 640

1921 CTGTCCATACATCAGGTCTATGGCAAAGAGGCTTGTATTCCATCGGGCCTGGGAGTAAA 1980
 641 L S I H Q V Y G K E A C I P C G P G S K 660

1981 AACAAATCAGGACCATTCCGTTTGTCTATAGTGACTGCTTTTTCTACCATGAAAAAGAAAAT 2040
 661 N N Q D H S V C Y S D C F F Y H E K E N 680

2041 CAGATTTTGCACCTATGACTTTAGCAACCTCAGCAGTGTGGGCTCATTAATGAATGGCCCC 2100
 681 Q I L H Y D F S N L S S V G S L M N G P 700

2101 AGCTTCACCTCCAAAGGAACAAAATACTTCCATTTCTTCAATATCAGTTTATGTGGGCAT 2160
 701 S F T S K G T K Y F H F F N I S L C G H 720

FIG. 4C



2161 GAGGGGAAGAAGATGGCTCTCTGTACCAACAATATAACAGACTTTACAGTAAAAGAAATA 2220
 721 E G K K M A L C T N N I T D E T V K E I 740
 2221 GTGCCAGGGTCAGATGATTACACAAATTTGGTAGGGGCATTGTATGCCAGTCAACAATT 2280
 741 V A G S D D Y T N L V G A F V C Q S T I 760
 2281 ATTCCTTCTGAAAGTAAGGGTTTCCGAGCAGCCTTATCATCACAATCCATCATTCTGGCA 2340
 761 I P S E S K G F R A A L S S Q S I I L A 780
 2341 GATACATTCATAGGAGTCACAGTTGAAACCACATTGAAAAATATTAATATAAAAGAAGAT 2400
 781 D T F I G V T V E T T L K N I N I K E D 800
 2401 ATGTTCCCAGTTCCAACAAGCCAAATACCAGATGTGCATTTCTTTTATAAGTCTTCTACA 2460
 801 M F P V P T S Q I P D V H F F Y K S S T 820
 2461 GCAACAACATCTTGTATTAATGGCCGATCAACTGCTGTGAAAATGAGGTGTAATCCTACT 2520
 821 A T T S C I N G R S T A V K M R C N P T 840
 2521 AAATCTGGAGCAGGAGTGATTTTCACTCCCCAGCAAGTGCCCAGCAGGTACCTGTGATGGG 2580
 841 K S G A G V I S V P S K C P A G T C D G 860
 2581 TGTACGTTCTATTTTCTGTGGAGAGTGCTGAAGCTTGCCCTCTGTGTACGGAGCATGAC 2640
 861 C T F Y F L W E S A E A C P L C T E H D 880
 2641 TTCCATGAGATTGAGGGAGCCTGCAAGAGAGGATTTTCAAGAAACCTTGTATGTGTGGAAT 2700
 881 F H E I E G A C K R G F Q E T L Y V W N 900
 2701 GAACCTAAATGGTGCATTAAAGGAATTTCTTTGCCTGAGAAAAAGTTGCCAACCTGTGAA 2760
 901 E P K W C I K G I S L P E K K L A T C E 920
 2761 ACGGTTGACTTTTGGCTGAAGGTGGGAGCCGGTGTGGGAGCTTTTACTGCCGTTTTGCTG 2820
 921 T V D F W L K V G A G V G A F T A V L L 940
 2821 GTGGCTCTGACCTGCTACTTCTGAAAAAGAATCAAAAAGTGAATACAAATATTCCAAG 2880
 941 V A L T C Y F W K K N Q K L E Y K Y S K 960

FIG. 4D



2881 TTAGTAATGACGACTAACTCAAAGAGTGTGAACTCCCGGCTGCAGACAGTTGTGCTATC 2940
 961 L V M T T N S K E C E L P A A D S C A I 980
 2941 ATGGAAGGAGAAGATAATGAAGAGGAAGTTGTATATTCCAATAAACAGTCACTACTAGGA 3000
 981 M E G E D N E E E V V Y S N K Q S L L G 1000
 3001 AAACTCAAATCTTTGGCAACCAAGGAAAAAGAAGACCATTTTGAATCTGTTCAACTGAAA 3060
 1001 K L K S L A T K E K E D H F E S V Q L K 1020
 3061 ACCTCAAGATCCCCAAATATATGAAGAGACAGTCTGTAGCCTTGAGACTAATGAACAAA 3120
 1021 T S R S P N I * 1028
 3121 GAAACCTGCTCTAGTTTTACAGGACCATATTTTAGGGTCTGTCTCATACCTGTCACATT 3180
 3181 GGTGATCTCACAGAGGAGGGCCATGCCGCTGAAAAGGGAAGGAGATTGAAACATTTGATT 3240
 3241 GCCTTATCACATGGTCAAGTACCTTGCCAAATAAAGGAAAGCAAATGATTGCGGTCTCAA 3300
 3301 CTGAAGATGAAGCTCAACTCAGGAAGAGATTTATCTGTATATACACATAACTGAAAACCA 3360
 3361 AGTTTAAGCCCACCAATGCACTGCTGATGCATGCCATATAATTAATGGGTAACCTTTTATT 3420
 3421 CTTTATGATGTCTACATAACAAGTGTGATTTGGAAGGCACATGTGAGCATATGCATTATG 3480
 3481 ATCCAATTTATGTTTTTCTTTGTTTATATTTTGGGAAAATTAAAATTTTTTTAAGGTA 3540
 3541 AAAAAAAAAAAAAA 3556

FIG. 4E



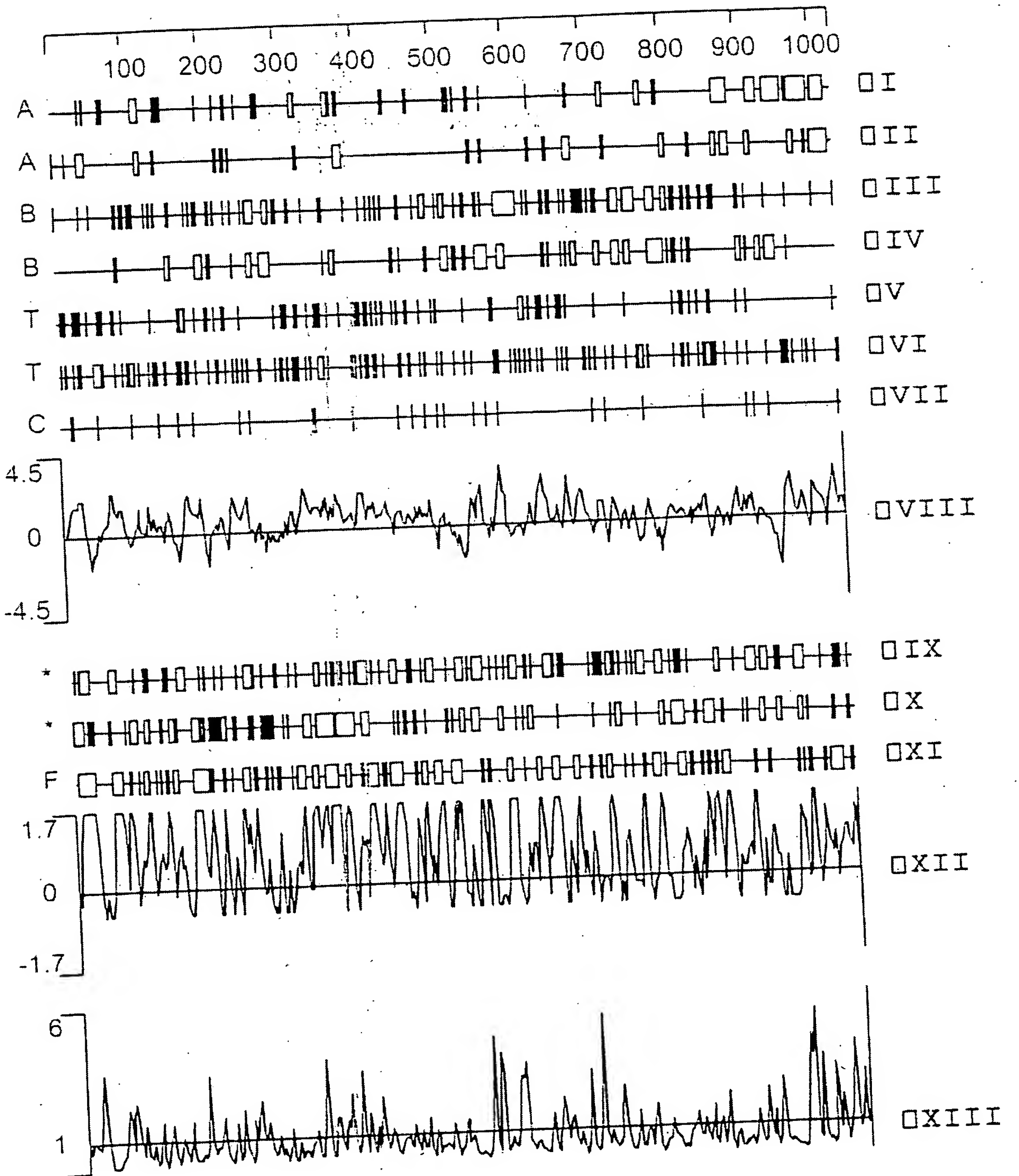
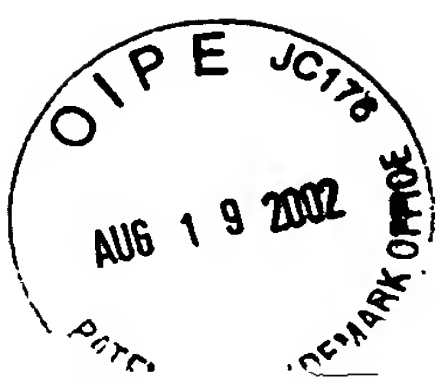


FIG. 5

	10	20	30	40																																										
1	M	L	F	R	A	R	G	P	V	R	G	R	G	W	G	R	P	A	E	A	P	R	R	G	R	S	P	P	W	S	P	A	W	I	C	C	W	A	L	A	SEQ ID 2					
1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	SEC10					
	50	60	70	80																																										
41	G	C	Q	A	A	W	A	G	D	L	P	S	S	S	S	R	P	L	P	P	C	Q	E	K	D	Y	H	F	E	Y	T	E	C	D	S	S	G	S	R	W	SEQ ID 2					
1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	SEC10					
	90	100	110	120																																										
81	R	V	A	I	P	N	S	A	V	D	C	S	G	L	P	D	P	V	R	G	K	E	C	T	F	S	C	A	S	G	E	Y	L	E	M	K	N	Q	V	C	SEQ ID 2					
1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	M	K	N	Q	V	C	SEC10
	130	140	150	160																																										
121	S	K	C	G	E	G	T	Y	S	L	G	S	G	I	K	E	D	E	W	D	E	L	P	A	G	E	S	N	I	A	T	E	M	D	T	V	V	G	P	S	SEQ ID 2					
7	S	K	C	G	E	G	T	Y	S	L	G	S	G	I	K	E	D	E	W	D	E	L	P	A	G	E	S	N	I	A	T	E	M	D	T	V	V	G	P	S	SEC10					
	170	180	190	200																																										
161	D	S	R	P	D	G	C	N	N	S	S	W	I	E	R	G	N	Y	I	E	S	N	R	D	D	C	T	V	S	L	I	Y	A	V	H	L	K	K	S	G	SEQ ID 2					
47	D	S	R	P	D	G	C	N	N	S	S	W	I	E	R	G	N	Y	I	E	S	N	R	D	D	C	T	V	S	L	I	Y	A	V	H	L	K	K	S	G	SEC10					
	210	220	230	240																																										
201	Y	V	F	F	E	Y	Q	Y	V	D	N	N	I	F	F	F	F	F	I	Q	N	D	C	Q	E	M	D	T	T	T	D	K	W	V	K	L	T	D	N	SEQ ID 2						
87	Y	V	F	F	E	Y	Q	Y	V	D	N	N	I	F	F	F	F	F	I	Q	N	D	C	Q	E	M	D	T	T	T	D	K	W	V	K	L	T	D	N	SEC10						
	250	260	270	280																																										
241	G	E	W	G	S	H	S	V	M	L	K	S	G	T	N	I	L	Y	W	R	T	T	G	I	L	M	G	S	K	A	V	K	P	V	L	V	K	N	I	T	SEQ ID 2					
127	G	E	W	G	S	H	S	V	M	L	K	S	G	T	N	I	L	Y	W	R	T	T	G	I	L	M	G	S	K	A	V	K	P	V	L	V	K	N	I	T	SEC10					
	290	300	310	320																																										
281	I	E	G	V	A	Y	T	S	E	C	F	P	C	K	P	G	T	F	S	N	K	P	G	S	P	N	C	Q	V	C	P	R	N	T	Y	S	E	K	G	A	SEQ ID 2					
167	I	E	G	V	A	Y	T	S	E	C	F	P	C	K	P	G	T	F	S	N	K	P	G	S	P	N	C	Q	V	C	P	R	N	T	Y	S	E	K	G	A	SEC10					
	330	340	350	360																																										
321	R	E	C	I	R	C	K	D	D	S	Q	F	S	-	-	G	S	S	E	C	T	E	R	P	P	C	T	T	K	D	Y	F	Q	I	H	T	P	C	D	E	SEQ ID 2					
207	R	E	C	I	R	C	K	D	D	S	Q	F	S	E	E	G	S	S	E	C	T	E	R	P	P	C	T	T	K	D	Y	F	Q	I	H	T	P	C	D	E	SEC10					
	370	380	390	400																																										
359	E	G	K	T	Q	I	M	Y	K	W	I	E	P	K	I	C	R	E	D	L	T	D	A	I	R	L	P	P	S	G	E	K	K	D	C	P	P	C	N	P	SEQ ID 2					
247	E	G	K	T	Q	I	M	Y	K	W	I	E	P	K	I	C	R	E	D	L	T	D	A	I	R	L	P	P	S	G	E	K	K	D	C	P	P	C	N	P	SEC10					
	410	420	430	440																																										
399	G	E	Y	N	N	G	S	S	S	C	H	E	C	P	P	G	T	F	S	D	G	T	K	E	C	R	P	C	P	A	G	T	E	P	A	L	G	F	E	Y	SEQ ID 2					
287	G	E	Y	N	N	G	S	S	S	C	H	E	C	P	P	G	T	F	S	D	G	T	K	E	C	R	P	C	P	A	G	T	E	P	A	L	G	F	E	Y	SEC10					
	450	460	470	480																																										
439	R	W	W	N	V	L	P	G	N	M	K	T	S	C	F	N	V	G	N	S	K	C	D	G	M	N	G	W	E	V	A	G	D	H	I	Q	S	G	A	G	SEQ ID 2					
327	R	W	W	N	V	L	P	G	N	M	K	T	S	C	F	N	V	G	N	S	K	C	D	G	M	N	G	W	E	V	A	G	D	H	I	Q	S	G	A	G	SEC10					
	490	500	510	520																																										
479	G	S	D	N	D	Y	L	I	L	N	L	H	I	P	G	E	K	P	P	T	S	M	T	G	A	T	G	S	E	L	G	R	I	T	F	V	F	E	T	L	SEQ ID 2					
367	G	S	D	N	D	Y	L	I	L	N	L	H	I	P	G	E	K	P	P	T	S	M	T	G	A	T	G	S	E	L	G	R	I	T	F	V	F	E	T	L	SEC10					

FIG. 6A



519	CSADCVLYEMVDINRRKSTNVVSWGGTKEKQAYTHIEPKN	SEQ ID 2
407	CSADCVLYEMVDINRRKSTNVVSWGGTKEKQAYTHIEPKN	SEC10
559	ATPTFTWAFQRTNQGGQDNRRFINDMVKIYSITATNAV DGV	SEQ ID 2
447	ATPTFTWGI PRE	SEC10
599	ASSCRACALGSEQSGSSCVPCPPGHYIEKETNQCKECP PD	SEQ ID 2
459		SEC10
639	TYLSIHQVYGKEACIPCGPGSGKNNQDHSVCYS DCFYHEK	SEQ ID 2
459		SEC10
679	ENQILHYDFS NLSSVGS LMN GPR SFTSKGT KY FEF FNISLC	SEQ ID 2
459		SEC10
719	GHEGKKMALCTNNITDFTVKEIVAGSDDYT NLVGA FVCQS	SEQ ID 2
464		SEC10
759	TIIPSESKGFRAALSSQSIILADTFIGVT VETTLKNINIK	SEQ ID 2
464		SEC10
799	EDMFVPVPTSQIPDVHFFYKSSTAT TSCINGRSTAVKMR CN	SEQ ID 2
464		SEC10
839	PTKSGAGVISVPSKCPAGTC DGCTFYFLWESAEACPLCTE	SEQ ID 2
464		SEC10
879	HDFHEIEGACKRGFQETLYVWNEPKWC IKGISLP EKKLAT	SEQ ID 2
464		SEC10
919	CETVD FWLKVGAGVGAF TAVLLVALTCYFWKKNQKKKKT I	SEQ ID 2
464		SEC10
959	LNLFN	SEQ ID 2
464		SEC10

Decoration 'Decoration #1': Shade (with solid black) residues that match the consensus named 'Consensus #1' exactly.

FIG. 6B



		10	20	30	40	
1	1	MLFRARGPVRGRGWGRPAZAPRRGRSPWPWSPAWICCWALA				SEQ ID 4
		-----				SEC10
		50	60	70	80	
41	1	GCQAAWAGDLPSSSSSRPLPPCQEKDYHFEYTECDSSGSRW				SEQ ID 4
		-----				SEC10
		90	100	110	120	
81	1	RVAIPNSAVDCSGLPDPVRGKECTFSCASGEYLE				SEQ ID 4
		-----MKNQVC				SEC10
		130	140	150	160	
121	7	SKCGEGTYSLSGSGIKEDWDDELPAGFSNIATFMDTVVGPS				SEQ ID 4
		SKCGEGTYSLSGSGIKFDWDDELPAGFSNIATFMDTVVGPS				SEC10
		170	180	190	200	
161	47	DSRFDGCNNSSWIFRGNYLESNRDDCTVSLIYAVHLKKS				SEQ ID 4
		DSRFDGCNNSSWIFRGNYLESNRDDCTVSLIYAVHLKKS				SEC10
		210	220	230	240	
201	37	YVFEFYQYVDNNIEFEFEFIQNDQCQEMDITTDKWKLT				SEQ ID 4
		YVFEFYQYVDNNIEFEFEFIQNDQCQEMDITTDKWKLT				SEC10
		250	260	270	280	
241	127	GEWGSHSVMLKSGTNILYWRRTTGILMGSKAVKPVLVKNIT				SEQ ID 4
		GEWGSHSVMLKSGTNILYWRRTTGILMGSKAVKPVLVKNIT				SEC10
		290	300	310	320	
281	167	IEGVAYTSECEPCKPGTFSNKPFGSPNCQVCPRNTYSEKGA				SEQ ID 4
		IEGVAYTSECEPCKPGTFSNKPFGSPNCQVCPRNTYSEKGA				SEC10
		330	340	350	360	
321	207	KECIRCKDDSQFS - GSSECTERPPCTTKDYEQIHTPCDE				SEQ ID 4
		KECIRCKDDSQFS EE GSSECTERPPCTTKDYEQIHTPCDE				SEC10
		370	380	390	400	
359	247	EGKTQIMYRWIEPKICREDLTDAILRPPSGEKKDCPPCNP				SEQ ID 4
		EGKTQIMYRWIEPKICREDLTDAILRPPSGEKKDCPPCNP				SEC10
		410	420	430	440	
399	287	GFYNGSSSCHPCPPGTFS DGTKECRPCPAGTEPALGPEY				SEQ ID 4
		GFYNGSSSCHPCPPGTFS DGTKECRPCPAGTEPALGPEY				SEC10
		450	460	470	480	
439	327	KWWNVLPFGNMKTSCFNVGNSKCDGMNGWEVAGDHIQSGAG				SEQ ID 4
		KWWNVLPFGNMKTSCFNVGNSKCDGMNGWEVAGDHIQSGAG				SEC10
		490	500	510	520	
479	367	GSDNDYLLILNLHIPGKEPPTSMTGATGSELGRITFVFETL				SEQ ID 4
		GSDNDYLLILNLHIPGKPPPTSMTGATGSELGRITFVFETL				SEC10

FIG. 7A



	530	540	550	560	
519	CSADCVLYEMVDINRRKSTNVVESWGGTKEKQAYTHIEKN				SEQ ID 4
407	CSADCVLYEMVDINRRKSTNVVESWGGTKEKQAYTHIEKN				SEC10
	570	580	590	600	
559	ATFTFTWAFQRTNQGDNRRFINDMVKIYSITATNAVDGV				SEQ ID 4
447	ATFTFTWGIPIRE				SEC10
	610	620	630	640	
599	ASSCRACALGSEQSGSSCVPCPPGHYIEKETNQCKECPD				SEQ ID 4
459					SEC10
	650	660	670	680	
639	TYLSIHQVYGKEACIPCGPGSKNNQDHSVCSDCFFYHEK				SEQ ID 4
459					SEC10
	690	700	710	720	
679	ENQILHYDFSNNLSSVGS				SEQ ID 4
459	LIQGP				SEC10
	730	740	750	760	
719	GHEGKKMALCTNNITDFTVKEIVAGSDDYTNLVGAFVCQS				SEQ ID 4
464					SEC10
	770	780	790	800	
759	TIIPSESKGFRAALSSQSIILADTFIGVTVETTLKNINIK				SEQ ID 4
464					SEC10
	810	820	830	840	
799	EDMFPVPTSQIPDVHFFYKSSTATTSCTINGRSTAVKMRCN				SEQ ID 4
464					SEC10
	850	860	870	880	
839	PTKSGAGVISVPSKCPAGTCDGCTFYFLWESAEACPLCTE				SEQ ID 4
464					SEC10
	890	900	910	920	
879	HDFHEIEGACKRGFQETLYVWNEPKWCIGISLPEKKLAT				SEQ ID 4
464					SEC10
	930	940	950	960	
919	CETVDFWLKVGAGVGAFVAVLLVALTCYFWKKNQKLEYKY				SEQ ID 4
464					SEC10
	970	980	990	1000	
959	SKLVMTTNSKECELPAAADSCAIMEGEDNEEEVVYSNKQSL				SEQ ID 4
464					SEC10
	1010	1020	1030		
999	LGKLSLATKEKEDHFESESVQLKTSRSPNI				SEQ ID 4
464				R	SEC10

Decoration 'Decoration #1': Shade (with solid black) residues that match the consensus named 'Consensus #1' exactly.

FIG. 7B

